

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 207

## (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

|   |     |
|---|-----|
| ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGTA ACACCAACCG CCGCCCTCAK   | 60  |
| GGSGTNNNNN NNCCGGGTGG CGGTCAGATC GTTSGTGGAG TTTACCTGTT GCCGCGCAGG   | 120 |
| GGCCCCAGGN NGGGTGTGGC CGCGACTAGG AAGACTTCCG AGCGGTCACA ACCTCGTGGC   | 180 |
| AGGCGACAGC CTATCCCCAA GGCTCGYCGG YCCGAGGGCA GGTCCCTGGGC TCAGCCCCGGG | 240 |
| TATCCTTGGC CCCTCTATGG CAATGAGGGC TGCGGGTGGG CGGGNTGGCT CCTGTCCCCC   | 300 |
| CGCGGCTCTC GGCCCAATIG GGGCCCC                                       | 327 |

## (2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

|   |  |
|---|--|
| Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn |  |
| 1 5 10 15   |  |
| Arg Arg Pro Xaa Xaa Xaa Xaa Pro Gly Gly Gly Gln Ile Val Gly     |  |
| 20 25 30  |  |
| Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Xaa Gly Val Arg Ala |  |
| 35 40 45  |  |
| Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro |  |
| 50 55 60  |  |
| Ile Pro Lys Ala Xaa Arg Xaa Glu Gly Arg Ser Trp Ala Gln Pro Gly |  |
| 65 70 75 80   |  |
| Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Xaa Trp |  |
| 85 90 95  |  |
| Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro             |  |
| 100 105   |  |

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 447 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GACGGCGTGA ACTATGCAAC AGGGAACITG CCCGTTGCT CTTTCTCTAT CTTCTCTTG 60  
 GCTTTGCTGT CCGTCTGAC GGTCCAACK ACCGCTCAG AGGTGCGCAA CGCATCCGGG 120  
 GTGTATCATG TCACCAACGA CTGTTCACAC TCGAGCATCA TCTATGAGAT GGACGGTATG 180  
 ATCATGCACT ACCCAGGGTG CGTGCCCTGC GTTCGGGAGG ATAACCATCT CCGCTGCTGG 240  
 ATGGCGCTCA CCCCCACGCT TGGGGTCAAA AAYGCTAGTG TCCCCACTRC GGCAATCCGA 300  
 CGTCACGTCG ACTTGCTTGT TGGGGNNCC ACGTCTCTTT CCGCTATGTA CGTGGGRCAC 360  
 CTTTGGGGGT CTGTCTTCTT CGCTGGCCAG CTATTACCT TTTACCCCG CATGCACCAT 420  
 ACAACGCAGG AGTGCAACTG CTCACATC 447

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 149 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser  
 1 5 10 15  
 Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Xaa Thr Ala  
 20 25 30  
 His Glu Val Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp Cys  
 35 40 45  
 Ser Asn Ser Ser Ile Ile Tyr Glu Met Asp Gly Met Ile Met His Tyr  
 50 55 60  
 Pro Gly Cys Val Pro Cys Val Arg Glu Asp Asn His Leu Arg Cys Trp  
 65 70 75 80  
 Met Ala Leu Thr Pro Thr Leu Ala Val Lys Xaa Ala Ser Val Pro Thr  
 85 90 95  
 Xaa Ala Ile Arg Arg His Val Asp Leu Leu Val Gly Xaa Xaa Thr Phe  
 100 105 110  
 Cys Ser Ala Met Tyr Val Xaa Asp Leu Cys Gly Ser Val Phe Leu Ala  
 115 120 125  
 Gly Gln Leu Phe Thr Phe Ser Pro Arg Met His His Thr Thr Gln Glu  
 130 135 140  
 Cys Asn Cys Ser Ile  
 145

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

|   |     |
|---|-----|
| ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGTA ACACCAACCG CGCCCCACAG | 60  |
| GACGTCAAGN TCCCGGGTGG TGCTCAGATC GTTGGTGGAG TTTACCTGTT GCCGCGCAGG | 120 |
| GGCCCCAGGT TGGGTGTGCG CGCGACCAGG AAGACTTCCG AGCGGTGCGA GCCTCGTGAC | 180 |
| AGCGGCACAG CTATTCCTAA GGCTCGCCAG TCCGATGGCA GNNCCTGGGC TCAGCCAGGG | 240 |
| CATCCCTGGC CCCTCTATGG CAATGAGGGC TCGGGATGGG CGGGATGGCT CCTGTCCCCC | 300 |
| CGCGGCTCTC GGCCCACTTG GGGCCCC                                     | 327 |

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 109 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

|   |  |
|---|--|
| Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn |  |
| 1 5 10 15   |  |
| Arg Arg Pro Gln Asp Val Lys Xaa Pro Gly Gly Gly Gln Ile Val Gly |  |
| 20 25 30  |  |
| Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala |  |
| 35 40 45  |  |
| Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Asp Arg Arg Gln Pro |  |
| 50 55 60  |  |
| Ile Pro Lys Ala Arg Gln Ser Asp Gly Xaa Xaa Trp Ala Gln Pro Gly |  |
| 65 70 75 80   |  |
| His Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp |  |
| 85 90 95  |  |
| Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro             |  |
| 100 105   |  |

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 447 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

|  |     |
|--|-----|
| GACGGCGTGA ACTATGCAAC AGGGAATTG CCTGGTTGCT CTTTCTCTAT CTTCCTCTTA   | 60  |
| GCTTTTCTGT CTGCTTGAC GGTTCCAACT ACCGCTCATG AGGTGCGCAA CGCATCCGGG   | 120 |
| GTATATCATC TCACCAATGA CTGTTCCAAC TCGAGCATCA TCTATGAGAT GAGTGGTIATG | 180 |

ATCTTGACAG CCCAGGGTG TGTGCCCTGC GTTCGGGAGA ACAACTCTTC TCGTTGCTGG 240  
 ATGCCRCCTCA CCCCCACGCT TCCGGTCAAA GACGCTAATG TCCCTACTGC GGCAATCCGA 300  
 CGCCATGTGC ACTTGCTGGT TGGGACAGCC GCGTTTCGTT CCGCTATGTA CGTGGGGGAC 360  
 CTCTGCGGAT CCGTCTTCCT TGTGGGCCAG CTATTCACCT TTTCACCCCG CTGTACCAT 420  
 ACAACACAGG AGTGCAACTG CTCAATC 447

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 149 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser  
 1 5 10 15  
 Ile Phe Leu Leu Ala Phe Leu Ser Cys Leu Thr Val Pro Thr Thr Ala  
 20 25 30  
 His Glu Val Arg Asn Ala Ser Gly Val Tyr His Leu Thr Asn Asp Cys  
 35 40 45  
 Ser Asn Ser Ser Ile Ile Tyr Glu Met Ser Gly Met Ile Leu His Ala  
 50 55 60  
 Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp  
 65 70 75 80  
 Met Xaa Leu Thr Pro Thr Leu Ala Val Lys Asp Ala Asn Val Pro Thr  
 85 90 95  
 Ala Ala Ile Arg Arg His Val Asp Leu Leu Val Gly Thr Ala Ala Phe  
 100 105 110  
 Arg Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val  
 115 120 125  
 Gly Gln Leu Phe Thr Phe Ser Pro Arg Leu Tyr His Thr Thr Gln Glu  
 130 135 140  
 Cys Asn Cys Ser Ile  
 145

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 223 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAAAGAA ACACCAACCG CGCCCCACAG 60  
 GACGTCAAGT TCCCGGGCGG TGGCCAGATC GTTGGTGCAG TCTACGTGCT ACCGCGCAGG 120  
 GGCCCTAGAT TGGGTGTGCG CGCAGCGCGG AAGACTTCGG AGCGGTGCA ACCTCGTGGG 180  
 AGCGGCCAAC CTATTCCTCAA GGAGCGCCGA CCCGAGGGCA GGT 223

[illegible]

(A) LENGTH: 74 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

(2) INFORMATION FOR SEQ ID NO: 11:

(A) LENGTH: 957 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

(2) INFORMATION FOR SEQ ID NO: 13:

(11) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

|  |     |
|--|-----|
| ATGAGCACAA ATCTTAACCC TCRAAGAAAA ACCAAAAGAA ATACCAACCG CCGCCCCACAG | 60  |
| GACGTCAAGT TCCCGGGCGG CGGCCAGATC GTTGGCGGAG TTTACTTGTT GCCGCGCAGG  | 120 |
| GGCCCCAGAT TGGGTGTGCG CGCGACGAGA AAGACTTCTG AACGGTCCCA GCCACGTGGA  | 180 |
| AGGCGCCAGC CCATCCCTAA AGATCGGNGN GCCACTGGCA GGTCCCTGGG ACGTCCAGGA  | 240 |
| TATCCCTGGC CCCTGTATGG GAACGAGGGG CTCGGCTGGG CAGGATGGCT CCTGTCCCCC  | 300 |
| CGAGGCTCTC   | 310 |

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

|   |     |     |    |    |
|---|-----|-----|----|----|
| Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn | 1   | 5   | 10 | 15 |
| Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly | 20  | 25  | 30 |    |
| Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala | 35  | 40  | 45 |    |
| Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro | 50  | 55  | 60 |    |
| Ile Pro Lys Asp Arg Xaa Ala Thr Gly Arg Ser Trp Gly Arg Pro Gly | 65  | 70  | 75 | 80 |
| Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp | 85  | 90  | 95 |    |
| Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly                 | 100 | 105 |    |    |

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 579 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

|   |     |
|---|-----|
| ACGTGCGGNT NTGCCGACCT CATGGGGTAC ATNCCCGTTG TCGGCGCCCC GGTGGGCGGG | 60  |
| GTNGCCAGGG CCCTCGCGNA TGGCGTGCGG GTCCTGGAGG ACGGGATAAA TTATGNAACA | 120 |
| GGAAACCTCC CTGGTTGCTC CTTTCTATC TTCTNGTTGG CTCTTCTGTC TTGTGTCACC  | 180 |
| GTGCTGTCT CTGNCGTGA GGTCAAAAAT ACCAGTCAGG CCTATATGGC AACCAACGAC   | 240 |
| TGCTCCAACA ACAGCATCGT ATGGCAATTG GNGACGCGG TGCTTCATGT TCCTGGATGT  | 300 |
| GTCCCTGCG AGAATAGCTC CGGTGCGTTC CACTGTTGGA TCCCGATCTC GCCCAACATA  | 360 |





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GGCCCCAGGT TGGGTGTGCG CGCGCCAAGG AAGACTTCTG AACGSTCCCA GCCACGTGGA 180
AGGCGCCAGC CCATCCCAA AGATCGGCGC GCCACTGGCA AGTCCTGGGG ACGTCCAGGA 240
TACCCCTTGC CCCTGTACGG GAACGAGGGC CTCGGCTGGG CAGGGTGGCT CCTGTCCCCC 300
CGGGGCTCTC GCCCCTCGTG GGGCCCAAAC GACCCCGGCG ACAGGTCAGG CAACTTGGGT 360
AAGGTCATCG ATACCCTCAC GTGTGGCTTT GSCGACCTCA TGGGGTACAT ACCTGTCGTC 420
GGCGCCCTTG TGGCGGCGGT TGCCAGAGCC CTCGCGCATG GCGTGCGGGT CCTGGAGGAC 480
GGGATAAATT ATGCAACAGG GAACTTGCCC GGTGCTCCT TTTCTATCTT CTGCTGGCT 540
CTCTTGCTTT GTATCACCCT GCCCGTGICT GCCATACAGG TTAAGAACAA CAGCCACTTC 600
TACATGGCGA CTAATGACTG TGCCAATGAC AGCATCGTCT GGCAGCTCAG GGACGCGGTG 660
CTCCATGTTT CTGGATGIGT CCCCTGTGAG AGGTCAGGTA ATAGGACCTT CTGTTGGACA 720
GGGCTCTCGC CCAACGTGGC TGTGAGCCGA CCTGGTGCTC TCACTAGAGG TCTGCGGGCT 780
CACATTGATA CCATCGTGAT GTCCGCCACC CTCGTCTCTG CCTATACAT AGGGGACCTA 840
TGCGGCGCTG TGATGATAGC AGCGCAAGTT GCCGTCGTCT CACCGCAATA CCATACTTTT 900
GTCCAGGAAT GCAACTGCTC CATATACCCA GGCCATATCA CAGGACATCG AATGGNN 957

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(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 319 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1          5          10          15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20          25          30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35          40          45
Pro Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50          55          60
Ile Pro Lys Asp Arg Arg Ala Thr Gly Lys Ser Trp Gly Arg Pro Gly
65          70          75          80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
85          90          95
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
100         105         110
Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115         120         125
Gly Phe Xaa Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val
130         135         140
Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
145         150         155         160
Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
165         170         175
Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Ala Ile
180         185         190
Gln Val Lys Asn Asn Ser His Phe Tyr Met Ala Thr Asn Asp Cys Ala
195         200         205

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Pro Gly Cys Val Pro Cys Glu Leu Gln Gly Asn Lys Ser Arg Cys Trp  
65 70 75 80

Ile Pro Val Thr Pro Asn Val Ala Val Asn Gln Pro Gly Ala Leu Thr  
85 90 95

Arg Gly Leu Arg Thr His Ile Asp Thr Ile Val Met Val Ala Thr Leu  
100 105 110

Cys Ser Ala Leu Tyr Ile Gly Asp Val Cys Gly Ala Val Met Ile Ala  
115 120 125

Ala Gln Val Val Ile Val Ser Pro Gln His His Asn Phe Ser Gln Asp  
130 135 140

Cys Asn Cys Ser Ile  
145

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 310 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

|   |            |     |
|---|------------|-----|
| ATGAGCACAA ATCCTAAACC TCAAAGAAAA ACCAAAAGAA AACTAACC  | CGCCCCACAG | 60  |
| GACGTTAAGT TCCCGGGCGG TGGCCAGATC GTTGGCGGAG TATACTTGT | GCCGCGCAGG | 120 |
| GGCCCCCGGT TGGGTGTGCG CGCGACGAGG AAAACTTCG ACGGTCCCA  | GCCACGTGGG | 180 |
| AGCGGCCAGC CCATCCCTAA AGATCGGCGC TCCACTGGCA AATCCTGGG | ACGTCCAGGA | 240 |
| TACCCTTGGC CCCTGTATGG GAACGAGGGC CTGGTTGGG CAGGATGGCT | CTGTCCCT   | 300 |
| CGAGGCTCTC  |            | 310 |

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

|   |  |
|---|--|
| Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn |  |
| 1 5 10 15   |  |
| Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Arg Ser Leu Ala |  |
| 20 25 30  |  |
| Glu Tyr Thr Cys Ala Arg Arg Gly Lys Leu Arg Arg Ser Ser Met Gly |  |
| 35 40 45  |  |

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 447 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

|   |     |
|---|-----|
| GACGGGATAA ACTATGCAAC AGGGAACCTG CCTGGTTGCT CTTTTCTAT CTTCCTACTG  | 60  |
| GOCCTGCTTT CTTCATCAC CGTGCCGGTC TCTGCCGTGC AAGTTCGAA CCGCAGTGGT   | 120 |
| TCTTACATGG TGACCAATGA TTGCTCGAAC AGCAGCATCG TTTGGCAGCT CGAGGAGGCC | 180 |
| GTCCCTCAGC TCCCTGGATG TGTCCCTGT GAGTGAAGG ACAACACCTC CCGCTGCTGG   | 240 |
| ATACCGGTCA CCCCTAACAT CGCTGTGAGC CAACCTGGCG CGCTTACCAA GGCCTGCGG  | 300 |
| ACACATATTG ACATCATGT CGCGTCCGCC ACGTTCTGCT CTGCCTTGTA TGTGGG      | 356 |

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

|   |     |     |     |    |
|---|-----|-----|-----|----|
| Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser | 1   | 5   | 10  | 15 |
| Ile Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Ala | 20  | 25  | 30  |    |
| Val Gln Val Ala Asn Arg Ser Gly Ser Tyr Met Val Thr Asn Asp Cys | 35  | 40  | 45  |    |
| Ser Asn Ser Ser Ile Val Trp Gln Leu Glu Glu Ala Val Leu His Val | 50  | 55  | 60  |    |
| Pro Gly Cys Val Pro Cys Glu Trp Lys Asp Asn Thr Ser Arg Cys Trp | 65  | 70  | 75  | 80 |
| Ile Pro Val Thr Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Xaa Thr | 85  | 90  | 95  |    |
| Lys Gly Leu Arg Thr His Ile Asp Ile Ile Val Ala Ser Ala Thr Phe | 100 | 105 | 110 |    |
| Cys Ser Ala Leu Tyr Val   | 115 |     |     |    |

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

|   |     |
|---|-----|
| ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGTA ACACCAACCG CCGCCCATG  | 60  |
| GACGTTAAGT TCCCGGGTGG TGGCCAGATC GTTGGCGGAG TTTACTTGTG GCCGCGCAGG | 120 |
| GGCCCCAGGT TGGGTGTGCG CGCGACTCGG AAGACTTCGG AGCGGTGCGA ACCTCTGGG  | 180 |
| AGACGCCAAC CTATCCCCAA GGCGCGTCGA TCCGAGGGAA GGTCTTGGG ACAGCCAGGA  | 240 |
| TATCCATGGC CTCTTTACGG TAATGAGGGT TGCGGGTGGG CANNATGGCT CTGTGCCCCC | 300 |
| CGCGGTTCTC  | 310 |

## (2) INFORMATION FOR SEQ ID NO: 28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1      5      10      15
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20      25      30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35      40      45
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50      55      60
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly
65      70      75      80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Xaa Trp
85      90      95
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
100     105     110
Arg Arg Arg Ser Arg
115

```

## (2) INFORMATION FOR SEQ ID NO: 29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```

GACGGGATCA ATTTTGCAAC AGGGAACCTC CCGGTTGCT CCTTTCTAT CTTCCTCTTG      60
GCACTCCTCT CGTGCTGAC TGTCCCGCT TCGGCCATCA ACTATCGCAA TGTCTCGGGC      120
ATTTACTATG TCACCAATGA TTGCCCCAAT TCAAGCATAG TGTATGAGGC CGACCATCAC      180
ATCTTGCAAC TCCAGGTTG CGTGCCCTGC GTGAGAGAGG GGAATCAGTC ACGTTGCTGG      240
GTAGCCCTTA CCCCTACCGT CGCAGCGCCA TACATCGGCG CGCCACTTGA GTCTCTACGG      300
AGTCATGTGG ACTTGATGGT GGGGGCCGCC ACTGTTTGT CAGCCCTTTA CATCGGGGAT      360
TTTGTGGYG GCTTGTTCCT AGTCGGTCAG ATGTTCTCTT TCCGACCAAG GCGCCACTGG      420
ACTACTCAAG ATTGCAATTG TTCCATC                                         447

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## (2) INFORMATION FOR SEQ ID NO: 30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser  
 1 5 10 15  
 Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala  
 20 25 30  
 Ile Asn Tyr Arg Asn Val Ser Gly Ile Tyr Tyr Val Thr Asn Asp Cys  
 35 40 45  
 Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His Leu  
 50 55 60  
 Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Gln Ser Arg Cys Trp  
 65 70 75 80  
 Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro Leu  
 85 90 95  
 Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val  
 100 105 110  
 Cys Ser Ala Leu Tyr Ile Gly Asp Xaa Cys Xaa Gly Leu Phe Leu Val  
 115 120 125  
 Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln Asp  
 130 135 140  
 Cys Asn Cys Ser Ile  
 145

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 447 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GACGGGATCA ATTATGCAAC AGGGAACCTT CCCGGTTGCT CTTTTCTAT CTTCCTCTTG 60  
 GCACCTCCTCT CGTGCCCTGAC TGTTCCCGCT TCGGCCATTA ACTACCGCAA CACCTCGGGC 120  
 ATCTACCACG TCACCAATGA CTGCCCGAAC TCGAGCATAG TTTATGAGGC CGACCACCAC 180  
 ATCTTGACAC TTCCAGGTTG CGTGCCCTGC GTGAGAAGTG GGAATCAGTC ACGTTGCTGG 240  
 GTGGGCCCTTA CTCCTACCGT CGCAGCGCCA TACATCGGCG CACCGCTTGA GTCTCTGCGG 300  
 AGTCATGTGG ATCTGATGGT GGGGGCTGCC ACTGTTTGCT CAGCCCTTGA CATCGGGGAT 360  
 TTGTGTGGCG GCTTGTCTCT GGTGAGTCAG ATGTTTCTT TCCGACCACG ACGCCACTGG 420  
 ACTGCCCAGG ATGCAATTG TTCTATC 447

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 149 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser  
 1 5 10 15





Ile Asn Tyr His Asn Thr Ser Gly Ile Tyr His Ile Thr Asn Asp Cys  
35 40 45

Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His Leu  
50 55 60

Pro Gly Cys Val Pro Cys Val Arg Val Gly Asn Gln Ser Ser Cys Trp  
65 70 75 80

Val Ala Leu Thr Pro Thr Ile Ala Ala Pro Tyr Ile Gly Ala Pro Leu  
85 90 95

Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val  
100 105 110

Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ala Phe Leu Val  
115 120 125

Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln Asp  
130 135 140

Cys Asn Cys Ser Ile  
145

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 447 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

|   |     |
|---|-----|
| GACGGGATCA ATTATGCAAC AGGGAATATT CCGGTTGCT CYTTTCTAT CTTCCTTYTG   | 60  |
| GCACTTCTCT CGTGTCTGAC TGTCCTCGCT TCGGCCACTA ACTATCGCAA CGTCTCGGGC | 120 |
| ATCTACCATG TCACCAATGA CTGCCCGAAT TCAAGCATAG TGTATGAGGC CGACCATCAC | 180 |
| ATCTTAGCAC TTCCAGGTTG CGTGCCCTGC GTGAGAGTGG GGRACCAGTC ACGTGCTGCG | 240 |
| GTGGCCCTTA CCCCTACCGT CGCAGCGCCA TACACGCGCG CGCCGCTTGA GTCCCTGCGG | 300 |
| AGTCATGTGG ATCTGATGGT GGGAGCTGCC ACTGTTTGT CAGCCCTTGA CATCGGGGAY  | 360 |
| TTGTGTGGCG GOTTGTTCTT GGTGGTCAG ATGTTCTCTT TYCAGCCTCG GCGCCACTGG  | 420 |
| ACTACCCAGG ATTGCAATTG TTCCATC                                     | 447 |

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 149 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Ile Pro Gly Cys Xaa Phe Ser  
1 5 10 15

Ile Phe Leu Xaa Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala  
20 25 30

Thr Asn Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys  
35 40 45

Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu Ala Leu

50                      55                      60

Pro Gly Cys Val Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys Trp  
65                      70                      75                      80

Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Thr Ala Ala Pro Leu  
                    85                      90                      95

Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val  
                    100                      105                      110

Cys Ser Ala Leu Tyr Ile Gly Xaa Leu Cys Gly Gly Leu Phe Leu Val  
                    115                      120                      125

Gly Gln Met Phe Ser Xaa Gln Pro Arg Arg His Trp Thr Thr Gln Asp  
                    130                      135                      140

Cys Asn Cys Ser Ile  
145

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 447 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GACGGGATTA ATTATGCAAC AGGGAAYCTC CCCGTTGCT CTTTCTCTAT CTTCCTCTTG      60

GCACCTTCTCT CGTGCCCTGAC TGTCCCGCT TCGGCCACCA ACTACCGCAA TGTCTCGGGC      120

ATTTACCATG TCACCAATGA CTGCCCGAAT TCAAGCATAG TGTTCGAGGC CGACCATCAC      180

ATCTTGACCC TTCCAGGATG CGTGCCCTGC GTGAAAGAGG GAAATCATTC ACGCTGCTGG      240

GTGGCCCTTA CCCCTACCGT CCGAGCCCCA TACATCGCGG CGCCACTTGA GTCTCTACGG      300

AGTCATGTGG ATGTGATGGT GGGGGCTGCC ACTGTTTGTG CAGCCCTTTA CATCGGGGAT      360

CTGTCCGGTG GCTTGTTCCT GGTGGGTCAG ATGTTCTCTT TCCGACCACG GCGCCACTGG      420

ACTACCCAGG AATGCAATTG TTCCATC      447

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 149 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Asp Gly Ile Asn Tyr Ala Thr Gly Xaa Leu Pro Gly Cys Ser Phe Ser  
1                      5                      10                      15

Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala  
                    20                      25                      30

Thr Asn Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys  
                    35                      40                      45

Pro Asn Ser Ser Ile Val Phe Glu Ala Asp His His Ile Leu His Leu  
                    50                      55                      60

Pro Gly Cys Val Pro Cys Val Lys Glu Gly Asn His Ser Arg Cys Trp  
65                      70                      75                      80

| Year | 1975 | 1976 | 1977 | 1978 | 1979 | 1980 | 1981 | 1982 | 1983 | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| 1975 | 1976 | 1977 | 1978 | 1979 | 1980 | 1981 | 1982 | 1983 | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 |      |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 149 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Gly | Ile | Asn | Tyr | Ala | Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Phe | Ile | Leu | Ala | Leu | Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | His | Tyr | Arg | Asn | Val | Ser | Gly | Ile | Tyr | His | Val | Thr | Asn | Asp | Cys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Asn | Ser | Ser | Ile | Val | Tyr | Glu | Ser | Asp | His | His | Ile | Leu | His | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Gly | Cys | Val | Pro | Cys | Val | Lys | Thr | Gly | Asn | Thr | Ser | Arg | Cys | Trp |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | Ala | Leu | Thr | Pro | Thr | Val | Ala | Ala | Pro | Ile | Leu | Ser | Ala | Pro | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |



Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala  
 35 40 45  
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60  
 Ile Pro Lys Val Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly  
 65 70 75 80  
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp  
 85 90 95  
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro  
 100 105 110  
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Xaa  
 115 120 125  
 Xaa Leu Ala Asp Leu Met Gly Tyr Ile Pro Val Leu Gly Gly Pro Leu  
 130 135 140  
 Gly Gly Val Ala Ala Ala Leu Ala His Gly Val Arg Ala Ile Glu Asp  
 145 150 155 160  
 Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile  
 165 170 175  
 Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Thr Pro Ala Ser Ala Ile  
 180 185 190  
 Gln Val Lys Asn Ala Ser Gly Ile Tyr His Leu Thr Asn Asp Cys Ser  
 195 200 205  
 Asn Asn Ser Ile Val Phe Glu Ala Glu Thr Met Ile Leu His Leu Pro  
 210 215 220  
 Gly Cys Val Pro Cys Ile Lys Ala Gly Asn Glu Ser Arg Cys Trp Leu  
 225 230 235 240  
 Pro Val Ser Pro Thr Leu Ala Val Pro Asn Ser Ser Val Pro Ile His  
 245 250 255  
 Gly Phe Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys  
 260 265 270  
 Ser Ala Met Tyr Ile Gly Asp Leu Cys Gly Ser Ile Ile Leu Val Gly  
 275 280 285  
 Gln Leu Phe Thr Phe Arg Pro Lys Tyr His Gln Val Thr Gln Asp Cys  
 290 295 300  
 Asn Cys Ser Xaa Asn Xaa Gly His Val Thr Gly His Arg Met Ala  
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 957 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATGAGCACAC TTCAAAGAAC CCAAGAGAAA ACCAAAAGAA ACACCATCCG CCGCCACAG 60  
 GACGTCAAGT TCCCGGGTGG CGGCCAGATC GTTGGTGGAG TCTACTTGCT GCCGCGCAGG 120  
 GGCCCGCGCT TGGGTGTGCG CGCGACGAGA AAGACTTCTG AACGGTCCCA GCCCAGAGGT 180  
 AGGCGCCAAC CAATACCCAA AGTGGCGCCAC CAAACGGGCC GTACCTGGGC CCAGCCCGGG 240





Arg Xaa Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Xaa  
115 120 125

Xaa Phe Ala Asp Leu Ile Glu Tyr Ile  
130 135

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 957 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

ATGAGCACAC TTCCAAAACC CCAAAGAAAA ACCAAAAGAA ACACAAACCG TCGCCCAATG 60  
GATGTCAAGT TCCCGGGCGG CGGTGAGATC GTTGGTGGAG TCTACTGTT ACCGCGCAGG 120  
GGCCCAAGTT TGGGTGTGCG CGCGACGAGG AAGACTTCGG AACGGTCCCA GGCCAGAGGT 180  
AGGGCCCAAC CAATACCCAA GTTGCGCCAG AACCAAGGCC GAACCTGGGC TCAGCCTGGG 240  
TACCCCTGGC CCCTTTATGG GAACGAGGGC TCGGCTGGG CGGGGTGGCT CTGTGCCCCC 300  
CGTGGCTCTC GCCCGGACTG GGGNCCCAAT GACCCCCGNN GGAGGTCCCG CAACCTGGGT 360  
AAGGTCATCG ACACCCCTAC TTGCGGCTTC GCGACCTCA TGGAGTACAT CCCTGTCGTT 420  
GGCGCCCCCC TTGGAGGCGT TCGGCGCGAA CTGGNACATG GTGTCAGGGC CATCGAGGAC 480  
GGGATAAACT ATGCAACAGG GAATCTTCCT GGTGCTCTT TCTCTATCTT CCWCTTGCCA 540  
CTTCTCTCGT GCCTCACCAC GCCTGCCTCC GCACTAAACT ATGCTAACAA GTCTGGGCTG 600  
TATCATCTAA CCAATGACTG CCCCATAGC AGCATTGTGT ATGAGCGGAA TGGCATGATC 660  
CTGCATCTCC CGGGTTGCGT CCCCTGCGTG AAGACCGGCA ACCTGACCAA GTGTTGGCTG 720  
TGGGCTCCCG CGACATTGGC GTTCCAGAAT CGGTGCGGTG CCATCAGGGG TGTCCCGGAG 780  
CACGTGGACC TCTTGGTGGG TGCTGCTGCG TTCTGCTCTG CCATGTACGT GGGCGACTTA 840  
TGGGCTGGGC TCTTCTCGT TGGGCACTG TTCACGTTC GACCCAGGAT GTATGAGATC 900  
GCCCAGGACT GCAACTGTTC CATCTATGCA GGCCACATCA CTGGGCACCG GATGGCG 957

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 319 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
1 5 10 15

Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala  
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Ala Arg Gly Arg Arg Gln Pro





(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 115 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
1 5 10 15

Xaa Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
20 25 30

Gly Val Tyr Val Leu Pro Arg Arg Gly Pro Gln Leu Gly Val Arg Ala  
35 40 45

Val Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Ser Arg Arg Gln Pro  
50 55 60

Ile Pro Arg Ala Arg Arg Thr Glu Gly Arg Ser Trp Ala Gln Pro Gly  
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp  
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro  
100 105 110

Arg Arg Arg  
115

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| GACGGAATTA | AITTCGCAAC  | AGGGAATTTA | CCTGGTTCCT | CTTTCTCTAT | CTTCCTCTCG | 60  |
| GCTTTGTTCT | CATGCTTGCT  | TACACCCACA | GCCGGGCTGG | AGTACCGTAA | TGCCTCCGGA | 120 |
| CTCTACATGG | TAACATAACGA | CTGCAGTAAC | GGTAGTATCG | TGTATGAGGC | CGGGGATATT | 180 |
| ATCCTCCACT | TACCTGGCTG  | TGTCCCTGCG | GTACGCTCTG | GCAATACATC | AAGATGCTGG | 240 |
| ATCCCTGTGA | GCCCYACCGT  | CGCCGTGAAG | TCGCCCTGCG | CCGCCACCGC | CTCTCTCCGC | 300 |
| ACGCACGTGG | ATATGATGGT  | GGGRGCGGCC | ACCCTATGCT | CAGCTCTCTA | CGTAGGAGAC | 360 |
| CTTTGTGGAG | CGCTATTTCCT | TGTYGGGCAG | GGGTTCTCAT | GGAGACATCG | CCAGCATTGG | 420 |
| ACTGTCCAGG | ACTGCAACTG  | TTCCATC    |            |            |            | 447 |

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

Glu Arg Leu Tyr Ile Gly Gly Xaa Leu Thr Asn Ser Lys Gly Gln Asn  
 35 40 45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys  
 50 55 60  
 Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Arg Ala Ala Cys Arg Ala  
 65 70 75 80  
 Ala Lys Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Val Ile Cys Glu Ser Ala Gly Val Glu Glu Asp Ala Ala Asn Leu Arg  
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CTCGACAGTT ACTGAGAACG ACATCCGTAC CGAGGRATCA ATCTATCAAT GTTGTGACTT 60  
 GGCCCCYAG GCGCGCAAGG CCATAAAGTC GCTCACCAG CGGCTGTACG TCGGGGGCCC 120  
 CCTAACCAAT TCAAAGGGGC AGAACTGCGG CTATCGTCGG TGTCGCGCTA GCGGCGTGCT 180  
 GACCACCAGC TCGGGCAACA CCTCACATG CTACTTGAAA GCCAGGGCGG CCTGTGAGC 240  
 TGCAAGCTC CAGGACTGCA CGATGCTCGT GTGCGGAGAC GACCTTGTCG TTATCTGTGA 300  
 GAGCGCGGGA GTCGAGGAGG ACGCGGCGAA CCTACGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Ser Thr Val Thr Glu Asn Asp Ile Arg Thr Glu Xaa Ser Ile Tyr Gln  
 1 5 10 15  
 Cys Cys Asp Leu Ala Xaa Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr  
 20 25 30  
 Glu Arg Leu Tyr Val Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn  
 35 40 45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys  
 50 55 60  
 Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Arg Ala Ala Cys Arg Ala  
 65 70 75 80  
 Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Val Ile Cys Glu Ser Ala Gly Val Glu Glu Asp Ala Ala Asn Leu Arg  
 100 105 110

[illegible]

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(11i) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Val

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 652 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```
CGTACAGCCT CCAGGACCCC CCTCCCGGG AGAGCCATAG TGGTCTGCGG AACCGGTGAG      60
TACACCGGAA TTGCCAGGAC GACCGGGTCC TTTCTTGGAT CAACCCGCTC AATGCCTGGA      120
GATTGGGGCG TGCCCCCGCA AGACTGCTAG CCGAGTAGTG TTGGGTGCGG AAAGGCCTTG      180
TGGTACTGCC TGATAGGGTG CTTCGGAGTG CCCCGGGAGG TCTCGTAGAC CGTGCACCAT      240
GAGCACGAAT CCTAAACCTC AARGAAAAAC CAAAAGAAAC ACCAACCGCC GCCCACAGGA      300
CGTCAAGTTC CCGGGCGGGTG GCCAGATCGT TGGTGGAGTC TACGTGCTAC CGCGCAGGGG      360
CCCTAGATTG GGTGTGCGCG CAGCGCGGAA GACTTCGGAG CGGTGCAAC CTCGTGGGAG      420
GCGCCAACTT ATTCCCAAGG AGCGCCGACC CGAGGGCAGG TCCTGGGCGC AGCCCGGGTA      480
CCCTTGGCCC CTCTATGGTA ACGAGGGCTG CGGGTGGGCA GGTNGGCTCC TGTCCCTCG      540
CGGCTCCCGT CTTAGTTGGG GTCCTACTGA CCCCCGGCGT AGGTCAACGA ATTTGGGTAA      600
GGTCATCGAT ACCCTCACGT GTTGNITCGC CGACCTCATG GGTACATAC CG      652
```

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1      5      10      15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20     25     30
Gly Val Tyr Val Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35     40     45
Ala Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50     55     60
Ile Pro Lys Glu Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln Pro Gly
65     70     75     80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Xaa
85     90     95
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
100    105    110
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115    120    125
Xaa Phe Ala Asp Leu Met Gly Tyr Ile Pro
130    135
```

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

| (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 61:                         |     |
|---|-----|
| CTCAACGGTC ACTGAAGCTG ATATCCGAAC AGAGGAGTCC ATATACCAAT GCTGTGACCT | 60  |
| GCACCCCGAA GCACGTGTAG CCATCAAGTC TTTGACTGAA AGGCTGTACG TCGGGGGGCC | 120 |
| CTTGACCAAT TCAAAAGGGG AGAACTGCGG CTATCGCAGA TGCCGTGCCA GCGGCGCTTT | 180 |
| GACAACCAGC TCGCGCAACA CCTCACCTG CTATATCAAG GCCCTAGCAG CCTGTAGAGC  | 240 |
| TGCCAAGCTC CAGGACTGCA CCATGCTCGT CTGTGGCGAC GACCTGGTCG TGATCTGCGA | 300 |
| GAGTGTAGGG ACCCAGGAGG ATGCGGCGAG CCTGCGAGCC                       | 340 |

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

{x1} SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```

Ser Thr Val Thr Glu Ala Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln
1          5          10          15          20
Cys Cys Asp Leu His Pro Glu Ala Arg Val Ala Ile Lys Ser Leu Thr
          20          25          30          35
Glu Arg Leu Tyr Val Gly Gly Pro Leu Thr Asn Ser Lys Gly Glu Asn
          35          40          45          50
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
          50          55          60          65
Gly Asn Thr Leu Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Arg Ala
65          70          75          80          85
Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
          85          90          95          100
Val Ile Cys Glu Ser Val Gly Thr Gln Glu Asp Ala Ala Ser Leu Arg
          100          105          110          115
Ala

```

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| NTCAACAGTC | ACTGAGAGTG | ATATCCGTAC  | AGAGGAGTCC | ATCTACCAAT | GCTGTGATCT | 60  |
| AGACCCCGAG | GCTCGCAAGG | CCATAAGGTC  | CCTCACAGAG | AGGCTTTATA | TCGGGGGTCC | 120 |
| CCTGACAAAC | TCAAAAGGGC | AGAACTGCGG  | CTACCGCCGA | TGCCGTGCAA | GCGGCGTCCT | 180 |
| GACGACTAGC | TGCGGCAACA | CCCTCACCTG  | TTACATAAAG | GCCAGGGCAG | CCTGTCGAGC | 240 |
| TGCGAAGCTC | CAGGATTGCT | CAATGCTCGT  | CTGTGGCGAC | GACCTTGTCT | TTATCTGCGA | 300 |
| GATCGAGGGG | NTCCANGAGG | ATCCGTGCGAN | NNNNNNNNNN |            |            | 340 |

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

```

Ser Thr Val Thr Glu Ser Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln
1          5          10          15          20
Cys Cys Asp Leu Asp Pro Glu Ala Arg Lys Ala Ile Arg Ser Leu Thr
          20          25          30
Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
          35          40          45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
          50          55          60
Gly Asn Thr Leu Thr Cys Tyr Ile Lys Ala Arg Ala Ala Cys Arg Ala
65          70          75          80
Ala Lys Leu Gln Asp Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val
          85          90          95
Val Ile Cys Glu Ile Glu Gly Xaa Xaa Glu Asp Pro Ser Xaa Xaa Xaa
100          105          110
Xaa

```

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(111) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| CGTAGACCGT | GCACCAATGAG | CACGAATCCT | AAACCTCAAA | GAAAAACCAA | ACGTAACATC  | 60  |
| AACCGCCGCC | CACAGGACGT  | CAGTTCCCG  | GGCGGTGGCC | AGATCGTCGG | TGGAGTTTAC  | 120 |
| CTGTTGCCGC | GCAGGGGCC   | TAGATTGGGT | GTGCGCGCGA | CTAGGAAGAC | TTCCGAGCGG  | 180 |
| TCGCAACCTC | GTGGGAGGCG  | ACAGCCTATC | CCCAAGGCTC | GCCGATCCGA | GGGCAAGTCC  | 240 |
| TGGGCTCAGC | CCGGGTACCC  | TTGGCCCCTC | TATGGCAATG | AGGGCATGGG | TTGGGCAGGG  | 300 |
| TGGCTCCTGT | CCCCCAATGG  | CTCCCGGCCT | AGTTGGGGCC | CTTCAGACCC | CCGGCGTAGG  | 360 |
| TCGCGTAATT | TGGGTAAGGT  | CATCGATACC | CTCACATGG  | GCTTCGCCGA | CCTCATGGGG  | 420 |
| TACATTCGCG | TCGTCGGCGC  | CCCCCTAGGG | GGCGTTGCCA | GGGCCCTIGC | GCAAGGCTTC  | 480 |
| CGGGATCTAC | CACGTCACCA  | ACGATTGTTT | CAATGGGAGC | ATTGTGTATG | AGGCGGAAGG  | 540 |
| CATGATCATG | CATCTCCCCG  | GGTGCGTGCC | CTGCGTTCGG | GAAGGTAATA | TCTCTCGTTG  | 600 |
| CTGGGTACCG | TTTTCCCCCA  | CGCTCGCAGC | CAGGAATGCT | AGCGTCCCCA | CTCAGGCAAT  | 660 |
| TCGGCGACAC | GTCGACTIGC  | TTGTTGGGGC | GGCCACACTC | TGTTCTGCTA | TGTATGTGGG  | 720 |
| GGACCTCTGT | GGGTCCGTCT  | TCCTCGTCGG | CCAACTGTTT | ACCTTCACAC | CCCCGCCAGNA | 780 |
| CTACACAGTG | CAAGACTGCA  | ATTGTTCCAT | CTACCCCGGC | CATATAACGG | G           | 831 |



(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Thr | Asn | Pro | Lys | Pro | Gln | Arg | Lys | Thr | Lys | Arg | Asn | Ile | Asn |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Arg | Pro | Gln | Asp | Val | Lys | Phe | Pro | Gly | Gly | Gly | Gln | Ile | Val | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Val | Tyr | Leu | Leu | Pro | Arg | Arg | Gly | Pro | Arg | Leu | Gly | Val | Arg | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Arg | Lys | Thr | Ser | Glu | Arg | Ser | Gln | Pro | Arg | Gly | Arg | Arg | Gln | Pro |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Pro | Lys | Ala | Arg | Arg | Ser | Glu | Gly | Arg | Ser | Trp | Ala | Gln | Pro | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Tyr | Pro | Trp | Pro | Leu | Tyr | Gly | Asn | Glu | Gly | Met | Gly | Trp | Ala | Gly | Trp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Leu | Ser | Pro | His | Gly | Ser | Arg | Pro | Ser | Trp | Gly | Pro | Ser | Asp | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Arg | Arg | Ser | Arg | Asn | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Phe | Ala | Asp | Leu | Met | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Gly | Val | Ala | Arg | Ala | Leu | Ala | Gln | Gly | Phe | Arg | Asp | Leu |     |     |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(11i) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| NNNNNNNGTC  | ACTGAGAGTG | ATATCCGIGT | CGAGGARTCA | ATTTACCAAT | GCTGTGACCT | 60  |
| GGCCCCCGAG  | GCTCGCGTAG | CCATAAAGTC | GCTCACTGAG | CGGCTATATG | TCGGGGGGCC | 120 |
| TCTCACCAC   | TCAAAAGGAC | AGAACTGCGG | CTATCGCCGG | TGCCGTGCGA | GCGGTGTGCT | 180 |
| GACTACTAGC  | TGCGGTAACA | CCCTCACATG | CTACCTGAAA | GCCGCCCGCG | CCTGTCGAGC | 240 |
| TGCAAAAGCTC | CGGGAATGCA | CAATGCTCGT | GTGTGGCGAC | GACCTCCTCG | TTATCTGTGA | 300 |
| GAGTGCGGGG  | GTCCAGGAGG | ATGCTGCAAG | CCTNNNNNNN |            |            | 340 |

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Xaa Xaa Val Thr Glu Ser Asp Ile Arg Val Glu Xaa Ser Ile Tyr Gln  
1 5 10 15  
Cys Cys Asp Leu Ala Pro Glu Ala Arg Val Ala Ile Lys Ser Leu Thr  
20 25 30  
Glu Arg Leu Tyr Val Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn  
35 40 45  
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys  
50 55 60  
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ala Ala Cys Arg Ala  
65 70 75 80  
Ala Lys Leu Arg Glu Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
85 90 95  
Val Ile Cys Glu Ser Ala Gly Val Gln Glu Asp Ala Ala Ser Xaa Xaa  
100 105 110  
Xaa

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CTCGACAGTC ACAGAGAGAG ATATAAGNAC TGAGGAGTCC ATATACCAGG CTTGTTTCCTT 60  
ACCCGAGCAG GCCAGAACTG CCATACACTC ATTGACTGAG AGACTCTACG TAGGAGGGCC 120  
CATGATGAAC AGCAAAGGGC ANTCCTGCGG ATACAGGCAT TGCCGCGCCA GCGGAGTGCT 180  
CACCACCACT ATGGGGAATA CCATCACGTG CTACATCAGG GGCCTAGCGG CTTGTAAAGC 240  
AGCAGGAATA GTGGCCCCCA CCATGCTGGT GTGCGCGCAT GACCTAGTTG TCATCTCAGA 300  
GAGTCAGGGA GTCGAGGAGG ACGACCGGAA CCTGANNNNN 340

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

Ser Thr Val Thr Glu Arg Asp Ile Xaa Thr Glu Glu Ser Ile Tyr Gln  
1 5 10 15  
Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr  
20 25 30  
Glu Arg Leu Tyr Val Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser  
35 40 45  
Cys Gly Tyr Arg His Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met

50 55 60  
 Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys Ala  
 65 70 75 80  
 Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Val Ile Ser Glu Ser Gln Gly Val Glu Glu Asp Asp Arg Asn Leu Xaa  
 100 105 110  
 Xaa

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CTCAACCGTC ACAGAGAGGG ATATAAGAAC TGAGGAGTCC ATATACCTGG CCTGCTCCTT 60  
 ACCCGAGCAG GCCCGGACTG CCATACATTC ATTAAGTGG AGACTTTACG TGGGAGGGCC 120  
 CATGATGAAC AGCAAAGGGC AGTCCTGCGG ATACAGGCGT TGCCGCGCTA GCGGAGTGCT 180  
 CACCACCAGT ATGGGGAACA CCATCACGTG TTATGTGAAA GCCCTCGCAG CTTGTAAAGC 240  
 TCGGGGCATT GTTGCCCCCA CGATGCTGGT GTGCGGCGAT GACCTGGTTG TCATCTCAGA 300  
 GAGTCAGGGG GCTGAGGAGG ACGAGCGAAA CCTGAGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu  
 1 5 10 15  
 Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr  
 20 25 30  
 Glu Arg Leu Tyr Val Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser  
 35 40 45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met  
 50 55 60  
 Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Leu Ala Ala Cys Lys Ala  
 65 70 75 80  
 Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Val Ile Ser Glu Ser Gln Gly Ala Glu Glu Asp Glu Arg Asn Leu Arg  
 100 105 110  
 Val

(2) INFORMATION FOR SEQ ID NO: 73:

[illegible]

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| CTCCACAGTC | GCGGAGAGAG | ACATCAGGAC | CGAGGAGTCC | ATTTACCTTG  | CCTGCTCCTT  | 60  |
| ACCCGAGCAA | GCCCGAACTG | CCATACATTC | ATTGACTGAG | AGACTTTIACG | TAGGAGGGCC  | 120 |
| CATGATGAAC | AGCAAGGGAC | AGTCCTGCGG | TTACAGACGT | TGCCGCGCCA  | GCGGAGTGCT  | 180 |
| CACCACCAGC | ATGGGGAATA | CCATCACATG | CTATGTGAAG | GCATTAGCTG  | CCTGCAAAAGC | 240 |
| TGCAGGCATC | GTTGCTCCCA | CGATGCTGGT | TTGTGGCGAC | GATCTGGTCA  | TCATCTCAGA  | 300 |
| GAGTCAGGGA | ACCGAGGAGG | ATGAGCGGAA | CCTGAGAGTC |             |             | 340 |

(2) INFORMATION FOR SEQ ID NO: 74:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

```

Ser Thr Val Ala Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu
1          5          10          15
Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr
20          25          30
Glu Arg Leu Tyr Val Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser
35          40          45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met
50          55          60
Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Ala Ala Cys Lys Ala
65          70          75          80
Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
85          90          95
Ile Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu Arg
100         105         110
Val

```

(2) INFORMATION FOR SEQ ID NO: 75:

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(211) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

|            |            |            |            |            |             |      |
|------------|------------|------------|------------|------------|-------------|------|
| CGNACANCCT | CCAGGCCCC  | CCCTCCCGG  | AGAGCCATAG | TGCTCTGCGG | AACCGGTGAG  | 60   |
| TACACCGGAA | TTGCCGGGAA | GACTGGGTCC | TTTCTTGGAT | AAACCCACTC | TATGCCCGGC  | 120  |
| CATTTGCGG  | TGCCCCCGCA | AGACTGCTAR | CCGAGTAGCG | TTGGGTTCGG | AAAGGCCCTTG | 180  |
| TGGTACTGCC | TGATAGGGTG | CTTGCGAGTG | CCCCGGGAGG | TCTCGTAGAC | CGTGCATCAT  | 240  |
| GAGCACAAAT | CCTAAACCTC | AAAGAAAAAC | CAAAGAAAC  | ACTAACCGCC | GCCCAACGGA  | 300  |
| CGTTAAGTTC | COGGCGCGTG | GCCAGATCGT | TGGCGGAGTA | TACTTGTGTG | CNTGCAGGGG  | 360  |
| NCCCAGGTNG | NGTNTATGCG | CAACGANGAA | GACTNCCGAA | CAGTCCCAGC | CACGTGGGAG  | 420  |
| GCGCCAGCCC | ATCCCGAAAG | ATCGGNGCAC | CACTGGCAAG | TCCTGGGGAC | GTCACAGATA  | 480  |
| TCCCTGGCCC | CTGTATGGGA | ACGAGGSCCT | CGGTTGGGCA | GGGTGGCTCC | TGTCCCCCG   | 540  |
| GGGCTCCCGC | CCGTTCATGG | GCCCCACGGA | CCCCCGGCAT | AGTCTCGCGA | ACTTGGGTAA  | 600  |
| GGTCATCGAT | ACCCTCACGT | NCGGCTTTNC | CGACCTCATG | GGGTACATTC | CCGTCGTTGG  | 660  |
| CGCCCCAGTA | GUNGCGCTCG | CCAGAGCTCT | CGCGCATGGC | GTGAGAGTCC | TGGAGGACGG  | 720  |
| GATAAACTAT | GAAACAGGGA | ACCTCCCCGG | TTGCTCTTTC | TCTATCTCCC | TCCTTGCTCT  | 780  |
| TCTGTCTGA  | ATTACCGNGC | CAGTTTCTGC | TGTGGAATC  | AAAAACACCA | GMAACACATA  | 840  |
| CATGGTGACT | AACGACTGTT | CAACAGYAG  | CATCACTGG  | CAGCTTNNGN | NCGCGGTGCT  | 900  |
| TCACGTTCC  | GGATGCGTCC | CCTGTGAACG | AGAGGGCAAC | AGTTCCCGGT | GCTGGATTCC  | 960  |
| AGTCACGCCC | RACGTAKNCG | TGAGCCGACC | TGGTGCCCTA | ACCGAGGGTT | TGCATCGCA   | 1020 |
| CATCGACACC | ATCGTAGCGT | CCGCAACATT | TTGTTCTGCC | CTCTACATAG | GGGATGTATG  | 1080 |
| TGGCGCGATA | ATGATAGCTG | CCCAAGTGGT | CATCGTCTCG | CCGGAGCATC | ATCACTTTGT  | 1140 |
| CCAGGACTGT | AACGTGTCCA | TCTACCCGGG | CCACATAACG | GGGCTTCGTA | TGTNG       | 1195 |

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 318 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Thr | Asn | Pro | Lys | Pro | Gln | Arg | Lys | Thr | Lys | Arg | Asn | Thr | Asn |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Arg | Pro | Gln | Asp | Val | Lys | Phe | Pro | Gly | Gly | Gly | Gln | Ile | Val | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Val | Tyr | Leu | Leu | Xaa | Cys | Arg | Xaa | Pro | Arg | Xaa | Xaa | Xaa | Cys | Ala |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Xaa | Lys | Thr | Xaa | Glu | Gln | Ser | Gln | Pro | Arg | Gly | Arg | Arg | Gln | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Pro | Lys | Asp | Arg | Xaa | Thr | Thr | Gly | Lys | Ser | Trp | Gly | Arg | Pro | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Tyr | Pro | Trp | Pro | Leu | Tyr | Gly | Asn | Glu | Gly | Leu | Gly | Trp | Ala | Gly | Trp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Leu | Leu | Ser | Pro | Arg | Gly | Ser | Arg | Pro | Ser | Trp | Gly | Pro | Thr | Asp | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | His | Arg | Ser | Arg | Asn | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Xaa |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Phe | Xaa | Asp | Pro | Met | Gly | Tyr | Ile | Pro | Val | Val | Gly | Ala | Pro | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

Xaa Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
 145 150 155 160  
 Gly Ile Asn Tyr Glu Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile  
 165 170 175  
 Ser Leu Leu Ala Leu Leu Ser Ile Thr Xaa Pro Val Ser Ala Val Glu  
 180 185 190  
 Ile Lys Asn Thr Xaa Asn Thr Tyr Met Val Thr Asn Asp Cys Ser Asn  
 195 200 205  
 Xaa Ser Ile Thr Trp Gln Leu Xaa Xaa Ala Val Leu His Val Pro Gly  
 210 215 220  
 Cys Val Pro Cys Glu Arg Glu Gly Asn Ser Ser Arg Cys Trp Ile Pro  
 225 230 235 240  
 Val Thr Pro Xaa Val Xaa Val Ser Arg Pro Gly Ala Leu Thr Glu Gly  
 245 250 255  
 Leu Arg Ser His Ile Asp Thr Ile Val Ala Ser Ala Thr Phe Cys Ser  
 260 265 270  
 Ala Leu Tyr Ile Gly Asp Val Cys Gly Ala Ile Met Ile Ala Ala Gln  
 275 280 285  
 Val Val Ile Val Ser Pro Glu His His His Phe Val Gln Asp Cys Asn  
 290 295 300  
 Cys Ser Ile Tyr Pro Gly His Ile Thr Gly Pro Arg Met Xaa  
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

ATCCACAGTC ACTGAAAGAG ACATCAGAGT TGAAGAGTCC GTTTATCTGT CCTGTTCACT 60  
 TCCCAGAGGAG GCCCGAGCTG CCATACACTC ACTAACTGAG AGGCTGTACG TGGGAGGTCC 120  
 CATGCAGAAC ASCAAGGGGC AATCCTGCGG ATACAGGCGC TGCCGCGCCA GCGGGGTGCT 180  
 CACCCTAGC ATGGGGAATA CTCTCACATG CTACTTGAAG GCCCAGGCGG CCTGCAGGGC 240  
 CGCGGGCATT GTTGCACCCA CAATGCTGGT GTGTGGCGAC GACCTGGTCG TCATCTCAGA 300  
 GAGTCAGGGG ACTGAGAGGG ACGAGAACAA CCGAGACCT 340

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Ser Val Tyr Leu  
 1 5 10 15  
 Ser Cys Ser Leu Pro Glu Glu Ala Arg Ala Ala Ile His Ser Leu Thr  
 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Gln Asn Ser Lys Gly Gln Ser  
 35 40 45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met  
 50 55 60  
 Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala  
 65 70 75 80  
 Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Val Ile Ser Glu Ser Gln Gly Thr Glu Arg Asp Glu Asn Asn Leu Arg  
 100 105 110  
 Pro

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

CTCAACAGTC ACCGAGAGGG ACATCAGGAA TGAGGAGTCC ATATTCCTGG CCTGCTCGTT 60  
 GCCCGAGGAG GCCCGGACTG TCATACATTC GCTCACTGAG AGACTCTACA TAGCCGGGCC 120  
 GATGATGAAC AGCAAAGGCC AGTCCTGTGG ATACAGGCGT TGTGCGGCCA GCGGGGTGTT 180  
 CACCACTAGC ATGGGCAATA CCATCACCTG CTATGTGAAA GCCATGGCAG CTTGCAGAGC 240  
 TGCCGGGATT GACGCCCCCA CAATGTGGT ATGTGGCGAC GACCTGGTGG TCATCTCAGA 300  
 GAGTCAGGGG ACCGAGGAGG ACGAGCGAAA TCTGAGACTC 340

(2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Ser Thr Val Thr Glu Arg Asp Ile Arg Asn Glu Glu Ser Ile Phe Leu  
 1 5 10 15  
 Ala Cys Ser Leu Pro Glu Glu Ala Arg Thr Val Ile His Ser Leu Thr  
 20 25 30  
 Glu Arg Leu Tyr Ile Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser  
 35 40 45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met  
 50 55 60  
 Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Met Ala Ala Cys Arg Ala  
 65 70 75 80  
 Ala Gly Ile Asp Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu Arg  
 100 105 110

[illegible]

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

(2) INFORMATION FOR SEQ ID NO: 82:

(11) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

Arg

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO



(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```
CTCCACTGTA ACCGAAAAGG ACATCAGGCC CGAGGAAGAG GTCTATCAGT GTTGTGACCT    60
GGAGCCCGAA GCTCGCAAGG TTATTACCGC CCTCACAGAA AGACTCTACG TGGGCGGCCC    120
CATGCACAAC AGCAAGGGAG ACCTTTGTGG GTATCGGAGA TGCCGCGCAA GCGGCGTCTA    180
CAGGACCAGC TTCGGAACA CACTGACGTG CTACCTCAA GCTCAGCTG CTATTAGAGC    240
GGCAGGGCTG AGAGACTGCA CCATGCTGGT TTGCGGTGAC GACTTGGTCG TCATCGCTGA    300
GAGCGATGGC GTAGAGGAGG ATAACCGAGC CCTCCNAGCC    340
```

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

```
Ser Thr Val Thr Glu Lys Asp Ile Arg Pro Glu Glu Glu Val Tyr Gln
1          5          10         15
Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr
20        25        30
Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
35        40        45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
50        55        60
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
65        70        75        80
Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85        90        95
Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Asn Arg Ala Leu Xaa
100       105       110
Ala
```

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

```
CTCCACGGTG ACTGAAAAGG ACATCAGGGT CGAGGAAGAG ATCTATCAAT GTTGTGACCT    60
GGARCCCGAA GCCCGCAAAG CAATATCCGC CCTCACAGAG AGRCTCTACT TGGGCGGCCC    120
CATGTATAAC AGCAAAGGGG AGCTCTGCGG GTATCGGAGG TGCCGCGCGA GCGGAGTGTA    180
CACCACAAGT TTCGGGAACA CAGTGACCTG CTATCTTAAG GCCACCGCAG CTACCAGGGC    240
TGCAGGCCTA AAAGACTGCA CCATGCTGGT CTGCGGTGAC GACTTGGTCG TCATCGCCGA    300
```

GAGCGAGGGC GTAGAGGAGG ATTCCCAACC CCTCCGAGCC

340

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln  
 1 5 10 15  
 Cys Cys Asp Leu Xaa Pro Glu Ala Arg Lys Ala Ile Ser Ala Leu Thr  
 20 25 30  
 Glu Xaa Leu Tyr Leu Gly Gly Pro Met Tyr Asn Ser Lys Gly Glu Leu  
 35 40 45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
 50 55 60  
 Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala  
 65 70 75 80  
 Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Val Ile Ala Glu Ser Glu Gly Val Glu Glu Asp Ser Gln Pro Leu Arg  
 100 105 110  
 Ala

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

CTCCACCGTA ACCGAAAGGG ACATCAGGGT CGAGGAGGAG GTCTATCAGT GTTGTGATCT 60  
 GGAGCCAGAG GCCCGCAAGG CAATATCCGC CTCACGGAG AGACTCTATG TGGGCGGTCC 120  
 CATGTTTAAC AGCAAGGGAG ACCTATGTGG CTACCGCAGG TGCCGCGCAA GCGGCGTCTA 180  
 CACCACCAGC TTCGGAACA CACTGACCTG CTACCTCAAG GCCACGGCCG CTACCAGAGC 240  
 GGCCGGCCTG AAGGATTGCA CAATGCTGGT TTGCGGGGAC GACCTGGTGG TCATCGCAGA 300  
 GAGCGATGGC GTGGACGAGG ACCGCCGAGC CCTCCAAGCT 340

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln

1                    5                    10                    15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Ser Ala Leu Thr  
                   20                    25                    30

Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly Asp Leu  
                   35                    40                    45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
                   50                    55                    60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala  
                   65                    70                    75                    80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
                   85                    90                    95

Val Ile Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Arg Ala Leu Gln  
                   100                    105                    110

Ala

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

|  |     |
|--|-----|
| CTCAACAGTC ACAGAGCGCG AIGTCCAGAC GGAGCATGAC ATCTACCAGT GCTGTAAGTT  | 60  |
| GGAGCCCCCA GCACGGACAG CCATCACATC GCTTACTGAC CGATTGTACT NCGGTGGTCC  | 120 |
| CATGTNTAAC TCTAAAGGTC AGGCATGTGG ATACCGTAGG TGCAGGGCCA GTGGCGTCTT  | 180 |
| GACCACCATC CTGGCCAATA CTCTGACTTG CTACTTGAAA GTCAGGCGGG CATGCAGAGC  | 240 |
| TGCCGGGCTG AAGGACTTTG ACATGTTGGT CTGCGGAGAC GACCTTGTCTG TTATTTCGGA | 300 |
| GAGTTTGGGG GTCTCGGAGG AACTAGTGC AOTGCCAGCT                         | 340 |

(2) INFORMATION FOR SEQ ID NO: 90:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Ser Thr Val Thr Glu Arg Asp Val Gln Thr Glu His Asp Ile Tyr Gln  
 1                    5                    10                    15

Cys Cys Lys Leu Glu Pro Ala Ala Arg Thr Ala Ile Thr Ser Leu Thr  
                   20                    25                    30

Asp Arg Leu Tyr Xaa Gly Gly Pro Met Xaa Asn Ser Lys Gly Gln Ala  
                   35                    40                    45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ile Leu  
                   50                    55                    60

Ala Asn Thr Leu Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala  
                   65                    70                    75                    80

Ala Gly Leu Lys Asp Phe Asp Met Leu Val Cys Gly Asp Asp Leu Val

85 90 95  
Val Ile Ser Glu Ser Leu Gly Val Ser Glu Asp Thr Ser Ala Leu Arg  
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

|   |     |
|---|-----|
| CTCGACAGTC ACCGAGCGCG ACATCCRCAC CGAGCAGCAC ATCTACCAAT GCTGCCAACT | 60  |
| TGACCCGGTG GCACGCAAGG CTATTACATC TCTGACTGAG CGGCTGTACT GCGGCGGGCC | 120 |
| CAIGATGAAC TCCCGTGGTC AATCATGTGG ATACCGTAGG TGCCGAGCCA GTGGCGTGCT | 180 |
| CACCACGAGC TTGGGCAATA CCCTAACATG CTATTTGAAA GCACAASCAG CGTGTAGGGC | 240 |
| AGCAAAGCTC AAAAATATG ACATGTTAGT CTGCGGAGAC GATCTAGTCG TTATCGCGGA  | 300 |
| GAGTGGAGGA GTCTCTGAGG ATGTTGACGC CCTGCGAGCA                       | 340 |

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

|   |  |
|---|--|
| Ser Thr Val Thr Glu Arg Asp Ile Xaa Thr Glu His Asp Ile Tyr Gln |  |
| 1 5 10 15   |  |
| Cys Cys Gln Leu Asp Pro Val Ala Arg Lys Ala Ile Thr Ser Leu Thr |  |
| 20 25 30  |  |
| Glu Arg Leu Tyr Cys Xaa Gly Pro Met Met Asn Ser Arg Gly Gln Ser |  |
| 35 40 45  |  |
| Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Leu |  |
| 50 55 60  |  |
| Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala |  |
| 65 70 75 80   |  |
| Ala Lys Leu Lys Asn Tyr Asp Met Leu Val Cys Gly Asp Asp Leu Val |  |
| 85 90 95  |  |
| Val Ile Ala Glu Ser Gly Gly Val Ser Glu Asp Val Asp Ala Leu Arg |  |
| 100 105 110   |  |

Ala

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```
CTCCTCCGTC  ACGGAGCGTG  ACATCCGCAC  TGAACACGAC  ATCTATCAGT  GCTGCCAATT      60
AGATCCGGTA  GCACGGAAAG  CCATTACATC  TCTTACTGAG  CGGCTGTACT  GCGGCGGCCC      120
CATGTACAAC  TCTCGAGGTC  AGTCATGTGG  GTACCGCAGG  TGCCGGGCTA  GTGGTGTCTT      180
CACCACAAGC  TTGGGCAACA  CCATGACATG  CTACCTGAAG  GCTCAGGCGG  CTTGTAGGGC      240
AGCRAAGCTC  AAAAAGTTTG  ACATGTTGGT  CTGCGGAGAC  GACCTAGTCG  TTATTGCTGA      300
GAGCGGAGGA  GTCCCTGAGG  ATGCCGGGGC  CCTGCGAGTC                                     340
```

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```
Ser Ser Val Thr Glu Arg Asp Ile Arg Thr Glu His Asp Ile Tyr Gln
1      5      10      15
Cys Cys Gln Leu Asp Pro Val Ala Arg Lys Ala Ile Thr Ser Leu Thr
20     25     30
Glu Arg Leu Tyr Cys Gly Gly Pro Met Tyr Asn Ser Arg Gly Gln Ser
35     40     45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Leu
50     55     60
Gly Asn Thr Met Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala
65     70     75     80
Xaa Lys Leu Lys Asn Phe Asp Met Leu Val Cys Gly Asp Asp Leu Val
85     90     95
Val Ile Ala Glu Ser Gly Gly Val Pro Glu Asp Ala Gly Ala Leu Arg
100    105    110
Val
```

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```
ATCCACAGTC  ACGGGGCGCG  ACATACGCAC  AGAACNAGAC  ATTTACCTGT  CCTGCCAGCT      60
CGACCCAGAG  GCCCGGAAAG  CCATAAAGTC  TCTCACTGAG  AGGCTCTATG  TCGGGGGCCC      120
TATGTACAAC  TCAAAGGGCC  AACTCTGTGG  TCAACGCCGA  TGCCGAGCAA  GCGGAGTACT      180
```

CCCCACAAGC ATGGGTAACA CCATCACATG CTTCTGAAG GCAACCGCCG CTTGCGGAGC 240  
AGCCGGCTTT ACAGATTATG ACATGTTGGT CTGCGGAGAC GATTGGTTG TCGTAACTGA 300  
GAGTGCTGGA GTCAACGAGG ATATCGCTAA CCTGCGAGCC 340

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

Ser Thr Val Thr Gly Arg Asp Ile Arg Thr Glu Xaa Asp Ile Tyr Leu  
1 5 10 15  
Ser Cys Gln Leu Asp Pro Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr  
20 25 30  
Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Leu  
35 40 45  
Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Met  
50 55 60  
Gly Asn Thr Ile Thr Cys Phe Leu Lys Ala Thr Ala Ala Cys Arg Ala  
65 70 75 80  
Ala Gly Phe Thr Asp Tyr Asp Met Leu Val Cys Gly Asp Asp Leu Val  
85 90 95  
Val Val Thr Glu Ser Ala Gly Val Asn Glu Asp Ile Ala Asn Leu Arg  
100 105 110  
Ala

(2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CTCCACTGTC ACTGAGCAGG ACATCAGGGT AGAAGTTTCC ATCTTTCAGG CCTGTGACCT 60  
CAAGGACGAG GCTAGGAGGG TGATAACTTC ACTCACGGAG CGGCTTACT GTGGTGGTCC 120  
TATGTTCAAC AGCAAGGGAC AACACTGCGG TTACCGCCGC TGCCGTGCTA GTGGGGTGCT 180  
ACCCACCAGC TTCGGGAACA CAATCACCTG TTACATCAA GCAAAGGCAG CTACCAAAGC 240  
TGCCGGAATT AAAAATCCAT CATTCCTTGT CTGCGGAGAT GACTTGGTGC TGATTGCTGA 300  
GAGTGCAGGG ATCGATGAGG ACAAGAGCGC CTTGAGAGCT 340

(2) INFORMATION FOR SEQ ID NO: 98:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

[illegible]

Ala

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

AAGCAAGGGG GTGGAGGAGG ACCAGCGGGA CCTACGAGTC 340

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu  
1 5 10 15

Ser Cys Gln Leu Pro Glu Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr  
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Glu Asn Ser Lys Gly Gln Ala  
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Leu  
50 55 60

Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Lys Ala Ala Cys Lys Ala  
65 70 75 80  
Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val  
85 90 95  
Val Ile Ser Glu Ser Lys Gly Val Glu Glu Asp Gln Arg Asp Leu Arg  
100 105 110  
Val

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 335 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CTCCACTGTC ACTGAGAGAG ACATACGAC AGAAGAATCC ATCTAYTGG CTGTCAATT 60  
GCCCGAAGAG GCCCGGAAGG CCATTAAATC ACTGACAGAG AGACTATACG TGGGCGGCCC 120  
GATGGAAAAC AGCAAAGGCC AGGCCTGCGG ATATAGGCGT TGCCGCGCAA GCGGGGTATT 180  
CACCACAAGC TTGGGGAACA CCATGAATTG TTACATCAAG GCCAARGCAG CTGTAAAGC 240  
YGCTGGCATT GTTGACCCGG TGATGCTCGT GTGCGGCGAC GACCTAGTGG TCATCTCAGA 300  
GAGCAAGGGG GTAGAGGAGG ACCAGCGAGA CCTAC 335

(2) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Xaa Xaa  
1 5 10 15  
Ala Cys Gln Leu Pro Glu Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr  
20 25 30  
Glu Arg Leu Tyr Val Gly Gly Pro Met Glu Asn Ser Lys Gly Gln Ala  
35 40 45  
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Leu  
50 55 60  
Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Xaa Ala Ala Cys Lys Xaa  
65 70 75 80  
Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val  
85 90 95  
Val Ile Ser Glu Ser Lys Gly Val Glu Glu Asp Gln Arg Asp Leu Xaa  
100 105 110  
Xaa

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```
CGTACAGCCT CCAGGACCCC CCCTCCCGGG AGAGCCATAG TGGTCTGCGG AACCGGTGAG      60
TACACCGGAA TTGCCGGGAA GACTGGGTCC TTTCTTGGAT TAACCCACTC TATGCCCGGA      120
GATTTGGGCG TGCCCCCGCA AGACTGCTAG CCGAGTAGCG TGGGTTCGCG AAAGGCCTTG      180
TGGTACTGCC TGATAGGGTG CTTGCGAGTG CCCCAGGAGG TCTCSTAGAC CGTGCACCAT      240
GAGCACAAGT CCTAAACCTC AAAGACAAAC CAAAAGAAAC ACCAACCGCC GCCCACAGGA      300
CGTTAAGTTC CCGGGCGGGT GCCAGATCGT TGGCGGGGTG TACTTGITGC CGCGCAGGGG      360
CCCCAGAGTG GGTGTGCGCG CGACGAGAAA GACCTCGGAG CGGTCCGAGC CGCGTGGGAG      420
GCGCCAACTT ATCCCAAGG TTAGGCGCAC CACCGGCCGT T                        461
```

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 74 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```
Met Ser Thr Asn Pro Lys Pro Gln Arg Gln Thr Lys Arg Asn Thr Asn
1          5          10          15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20          25          30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Val Gly Val Arg Ala
35          40          45
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50          55          60
Ile Pro Lys Val Arg Arg Thr Thr Gly Arg
65          70
```

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```
CTCTACTGTC ACAGAGAGGG ATATACGAAC AGAGGAATCC ATYTATCTGG CTGTCAATT      60
GCCCCAAGAG GCCCGGAAGG CCATCAAAATC ACTGACAGAG AGACTATACG TGGGCGGCCC      120
GATGGAAGAC AGCAAGGGCC AGGCCTGCGG ATACAGGCGT TGCCGCGCAA GCGGGGIATT      180
```



(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

Glu Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

Ala Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

Asp Arg Arg Thr Thr Gly Lys Ser Trp Gly Arg  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

Asp Arg Arg Ala Thr Gly Arg Ser Trp Gly Arg  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Asp Arg Arg Ala Thr Gly Lys Ser Trp Gly Arg  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

106050" 8E T 6966

Val Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Val Arg His Gln Thr Gly Arg Thr Trp Ala Gln  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

Val Arg Gln Asn Gln Gly Arg Thr Trp Ala Gln  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

Ala Arg Arg Thr Glu Gly Arg Ser Trp Ala Gln  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 118:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

Val Arg Arg Thr Thr Gly Arg Xaa Xaa Xaa Xaa  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 119:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

Val Arg Arg Thr Thr Gly Arg Thr Trp Ala Gln  
1 5 10

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(2) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

His Glu Val Arg Asn Ala Ser Gly Val Tyr His Val  
 1                    5                    10

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

His Glu Val Arg Asn Ala Ser Gly Val Tyr His Leu  
 1                    5                    10

(2) INFORMATION FOR SEQ ID NO: 122:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

Tyr Glu Val His Ser Thr Thr Asp Gly Tyr His Val  
 1                    5                    10

(2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

Val Glu Val Lys Asn Thr Ser Gln Ala Tyr Met Ala  
 1                    5                    10

(2) INFORMATION FOR SEQ ID NO: 124:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

Ile Gln Val Lys Asn Asn Ser His Phe Tyr Met Ala  
 1                    5                    10

(2) INFORMATION FOR SEQ ID NO: 125:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

(2) INFORMATION FOR SEQ ID NO: 126:

(ii) MOLECULE TYPE: peptide

(2) INFORMATION FOR SEQ ID NO: 127:

(11) MOLECULE TYPE: peptide

(2) INFORMATION FOR SEQ ID NO: 128:

(11) MOLECULE TYPE: peptide

(2) INFORMATION FOR SEQ ID NO: 129:

(11) MOLECULE TYPE: peptide

(2) INFORMATION FOR SEQ ID NO: 130:

(ii) MOLECULE TYPE: peptide

[illegible]

Ile Asn Tyr Arg Asn Thr Ser Gly Ile Tyr His Val  
1 5 10

Ile Asn Tyr His Asn Thr Ser Gly Ile Tyr His Ile  
1 5 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

Thr Asn Tyr Arg Asn Val Ser Gly Ile Tyr His Val  
1 5 10

(ii) MOLECULE TYPE: peptide





- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

Val Tyr Glu Ala Lys Asp Ile Ile Leu His Thr  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

Val Trp Gln Leu Xaa Asp Ala Val Leu His Val  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

Val Trp Gln Leu Arg Asp Ala Val Leu His Val  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO: 144:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

Ile Trp Gln Met Gln Gly Ala Val Leu His Val  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO: 145:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

Val Trp Gln Leu Lys Asp Ala Val Leu His Val  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO: 146:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

Val Trp Gln Leu Glu Glu Ala Val Leu His Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

Thr Trp Gln Leu Xaa Xaa Ala Val Leu His Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

Val Tyr Glu Ala Asp His His Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

Val Tyr Glu Ala Asp His His Ile Leu Ala Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

Val Phe Glu Ala Asp His His Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

Val Tyr Glu Ser Asp His His Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Val Phe Glu Glu Thr Met Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

Val Tyr Glu Ala Glu Thr Leu Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

Val Tyr Glu Ala Asn Gly Met Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

Val Tyr Glu Ala Gly Asp Ile Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

Val Arg Glu Asp Asn His Leu Arg Cys Trp Met Ala Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 157:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Met Ala Leu  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO: 158:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

Ile Arg Glu Gly Asn Ile Ser Arg Cys Trp Val Leu Pro  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

Glu Asn Ser Ser Gly Arg Phe His Cys Trp Ile Pro Ile  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO: 160:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

Glu Arg Ser Gly Asn Arg Thr Phe Cys Trp Thr Ala Val  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO: 161:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

Glu Leu Gln Gly Asn Lys Ser Arg Cys Trp Ile Pro Val  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO: 162:

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Glu Arg His Gln Asn Gln Ser Arg Cys Trp Ile Pro Val  
1                    5                    10

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

(2) INFORMATION FOR SEQ ID NO: 164:

(ii) MOLECULE TYPE: peptide

Glu Arg Glu Gly Asn Ser Ser Arg Cys Trp Ile Pro Val  
1 5 10

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

(2) INFORMATION FOR SEQ ID NO: 166:

(ii) MOLECULE TYPE: peptide

Val Arg Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu  
1                      5                      10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:  
 Val Arg Val Gly Asn Gln Ser Ser Cys Trp Val Ala Leu  
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 168:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: peptide  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:  
 Val Arg Val Gly Asn Gln Ser Arg Cys Trp Val Ala Leu  
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 169:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: peptide  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:  
 Val Lys Glu Gly Asn His Ser Arg Cys Trp Val Ala Leu  
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 170:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: peptide  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:  
 Val Lys Thr Gly Asn Thr Ser Arg Cys Trp Val Ala Leu  
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 171:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: peptide  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:  
 Ile Lys Ala Gly Asn Glu Ser Arg Cys Trp Leu Pro Val  
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 172:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: peptide  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:



(2) INFORMATION FOR SEQ ID NO: 178:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

Val Ser Lys Pro Gly Ala Leu Thr Lys Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

Val Ser Arg Pro Gly Ala Leu Thr Arg Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

Val Asn Gln Pro Gly Ala Leu Thr Arg Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 181:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

Val Ser Gln Pro Gly Ala Leu Thr Arg Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 182:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Val Ser Gln Pro Gly Ala Leu Thr Lys Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 183:

- (i) SEQUENCE CHARACTERISTICS:





(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Val Pro Asn Ala Ser Thr Pro Val Thr Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

Val Gln Asn Ala Ser Val Ser Ile Arg Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Val Lys Ser Pro Cys Ala Ala Thr Ala Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

Ser Pro Arg Met His His Thr Thr Gln Glu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Ser Pro Arg Leu Tyr His Thr Thr Gln Glu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

Thr Ser Arg Arg His Trp Thr Val Gln Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 194:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Ala Pro Lys Arg His Tyr Phe Val Gln Glu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

Ser Pro Gln Tyr His Thr Phe Val Gln Glu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 196:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Ser Pro Gln His His Asn Phe Ser Gln Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

Ser Pro Gln His His Ile Phe Val Gln Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Ser Pro Glu His His His Phe Val Gln Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

Arg Pro Arg Arg His Trp Thr Thr Gln Asp  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO: 200:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

Arg Pro Arg Arg His Trp Thr Ala Gln Asp  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

Gln Pro Arg Arg His Trp Thr Thr Gln Asp  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Arg Pro Arg Arg His Trp Thr Thr Gln Glu  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

Gln Pro Arg Arg His Trp Thr Val Gln Asp  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO: 204:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids

199 200 201 202 203 204

**E**

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Arg Pro Lys Tyr His Gln Val Thr Gln Asp  
1                  5                  10

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | His | Arg | Gln | His | Trp | Thr | Val | Gln | Asp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |